

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Jun 05 18:58:10 EDT 2007

Reviewer Comments:

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (2)..(4)

<223> Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

The above <222> response denotes Xaa's at locations 2 through 4; however, "Pro" is at location 3. Same type of error throughout sequence 3 and sequence 43.

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

The <213> response above is erroneous; the response should only show "Homo sapiens." Please move "bromodomain peptide" to the <220>-<223> section.

<210> 34

<211> 112

<212> PRT

<213> Description of unknown organism, see Jeanmougin et al.,
Trends in Biochem. Sci. 22:151-153 (1997)

Per 1.823 of Sequence Rules, the only valid <213> response is "Unknown"; do not include any other explanation on the <213> line. The "see Jeanmougin..." is not a valid explanation of "Unknown." Please give the source of the genetic material in the <220>-<223> section. Same error in sequence 35.

Application No: 09510314 Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-05 17:13:10.137
Finished: 2007-06-05 17:13:14.253
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 116 ms
Total Warnings: 6
Total Errors: 19
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

Input Set:

Output Set:

Started: 2007-06-05 17:13:10.137
Finished: 2007-06-05 17:13:14.253
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 116 ms
Total Warnings: 6
Total Errors: 19
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)

SEQUENCE LISTING

<110> Zhou, Ming-Ming
Aggarwal, Aneel

<120> Methods of Identifying Modulators of Bromodomains

<130> 2459-1-003

<140> 09510314

<141> 2007-06-05

<150> 09/510,314

<151> 2000-02-22

<160> 44

<170> PatentIn version 3.0

<210> 1

<211> 3014

<212> DNA

<213> Homo sapiens

<400> 1

ggggccgcgt	cgacgcggaa	aagaggccgt	ggggggcctc	ccagcgctgg	cagacaccgt	60
gaggctggca	gcccgcggca	cgcacacaccta	gtccgcagtc	ccgaggaaca	tgtccgcagc	120
cagggcgcgg	agcagagtc	cgggcaggag	aaccaaggga	gggcgtgtgc	tgtggcgccg	180
gcggcagcgg	cagcgcagcc	gctagtc	tccctctgg	gggagcagct	gccgcgcgtg	240
ccgcgcgcgc	caccaccatc	agcgcgcggg	gcccgccag	agcgcgcgg	gcgcgcggcg	300
cgctaggggg	agggcggggg	cggggagggg	ggtggcgaa	gggggcggga	gggcgtgggg	360
ggagggtctc	gtctcccgaa	ctaccagac	ccgagggaga	ccctggcgcc	ggcggcgccg	420
cctgacactc	ggcgctctct	gccgtgtcc	ggggcgcat	gtccgaggtct	ggcgccgcgg	480
ggccggggccg	ctgcggggca	ggagccgggg	cagggggccgg	gcccgccggcg	ctgccccccgc	540
agcctgcggc	gcttcgcccc	gcccggccgc	agggctcccc	ctgcgcgcgt	gccgcgggggg	600
gctcgccgc	ctgcggtccg	gcaacggcag	tggctgcagc	gggcacggcc	gaaggaccgg	660
gaggcgggtgg	ctcgccccga	atgcgcgtga	agaaagcga	actacgtcc	gtccgcgggg	720
ccaagaaact	ggagaaactc	ggagtgtact	ccgcctgcaa	ggccgaggag	tcttgtaaat	780
gtaatggctg	aaaaaacct	aacccctac	ccactcccc	cagagccac	ctgcagcaaa	840
taattgtcag	tctaacagaa	tcctgtcgga	gtttagcca	tgccttagct	gctcatgttt	900
cccacctgga	aatgtgtca	gaggaagaaa	tgaacagact	cctggaaata	gtattggatg	960
tggaaatatct	ctttacctgt	gtccacaagg	aagaagatgc	agataccaaa	caagtttatt	1020
tctatctatt	taagctcttgc	agaaagtcta	ttttacaag	aggaaaacct	gtggttgaag	1080
gtctttggaa	aaagaaaccc	ccatttgaaa	aacctagcat	tgaacagggt	gtgaataact	1140
ttgtgcagta	caaatttagt	cacctgccag	caaaagaaag	gcaaacaata	gttgagttgg	1200
caaaaatgtt	cctaaaccgc	atcaactatt	ggcatctgga	ggcaccatct	caacgaagac	1260
tgcgatctcc	aatgtatgt	atttctggat	acaaagagaa	ctacacaagg	tggctgtgtt	1320
actgcaacgt	gccacagttc	tgcgacagtc	tacctcggt	cgaaaccaca	caggtgtttg	1380
ggagaacatt	gcttcgctcg	gtcttcactg	ttatgaggcg	acaactcctg	gaacaagcaa	1440
gacaggaaaa	agataaaactg	cctcttgaaa	aacgaactct	aatcctcact	catttcccaa	1500
atttctgtc	catgctagaa	gaagaagtat	atagtcaaaa	ctctcccatc	tggatcagg	1560
atttctctc	agccttcc	agaaccagcc	agctaggcat	ccaaaacagtt	atcaatccac	1620
ctcctgtggc	tggacaatt	tcatacaatt	caacctcatc	ttcccttgag	cagccaaacg	1680
cagggagcag	cagtctgcc	tgcaaagcct	cttctggact	tgaggcaaac	ccagggagaaa	1740
agaggaaaaat	gactgattct	catgttctgg	aggaggccaa	gaaaccccgaa	gttatgggggg	1800
atattccgat	ggaattaatc	aacgagggtta	tgtctaccat	cacggaccct	gcagcaatgc	1860
ttggaccaga	gaccaatttt	ctgtcagcac	actcgccag	ggatgaggcg	gcaagggttgg	1920

aagagcgcag	gggtgtatt	gaatttcacg	tggttggca	ttccctcaac	cagaaacc	1980
acaagaagat	cctgatgtgg	ctgggtggcc	tacagaacgt	tttctccac	cagctgccc	2040
gaatgccaaa	agaatacatac	acacggctcg	tctttgaccc	gaaacacaaa	acccttgctt	2100
taattaaaga	tggccgtgtt	attggtggtt	tctgtttccg	tatgttccca	tctcaaggat	2160
tcacagagat	tgtcttctgt	gctgtaacct	caaatgagca	agtcaagggc	tatgaaacac	2220
acctgatgaa	tcatttgaaa	gaatatcaca	taaagcatga	catcctgaac	ttcctcacat	2280
atgcagatga	atatgcaatt	ggatactta	agaaacaggg	tttctccaaa	gaaattaaaa	2340
taacctaaaac	caaatatgtt	ggctatatac	aggattatga	aggagccact	ttaatgggat	2400
gtgagctaaa	tccacggatc	ccgtacacag	aattttctgt	catcattaaa	aagcagaagg	2460
agataattaa	aaaactgatt	gaaagaaaaac	aggcacaaat	tcgaaaagtt	tacccctggac	2520
tttcatgttt	taaagatgga	gttcgacaga	ttccatataga	aagcattcct	ggaatttagag	2580
agacaggctg	gaaaccgagt	ggaaaagaga	aaagtaaaga	gcccgagagac	cctgaccagc	2640
tttacagcac	gctcaagagc	atccctccagc	aggtgaagag	ccatcaaagc	gcttggccct	2700
tcatggaaacc	tgtgaagaga	acagaagctc	caggatatta	tgaagttata	aggttcccc	2760
tggatctgaa	aaccatgagt	gaacgcctca	agaataggtt	ctacgtgtct	aagaaattat	2820
tcatggcaga	cttacagcga	gtctttacca	attgcaaaga	gtacaacgccc	gctgagagtg	2880
aataactacaa	atgtgcaat	atccctggaga	aatttttctt	cagtaaaatt	aaggaagctg	2940
gattaatgta	caagtgtattt	tttttcccc	tctgcttctt	agaaactcac	caagcagtgt	3000
gccttaaagca	aggt					3014

<210> 2
<211> 832
<212> PRT
<213> Homo sap

<400> 2

Met Ser Glu Ala Gly Gly Ala Gly Pro Gly Gly Cys Gly Ala Gly Ala
1 5 10 15

Gly Ala Gly Ala Gly Pro Gly Ala Leu Pro Pro Pro Gln Pro Ala Ala Leu
20 25 30

Pro Pro Ala Pro Pro Gln Gly Ser Pro Cys Ala Ala Ala Ala Gly Gly
35 40 45

Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Ala Gly Thr Ala
50 55 60

Glu Gly Pro Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala
65 70 75 80

Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val
85 90 95

Tyr Ser Ala Cys Lys Ala Glu Glu Ser Cys Lys Cys Asn Gly Trp Lys
 100 105 110

Asn	Pro	Asn	Pro	Ser	Pro	Thr	Pro	Pro	Arg	Ala	Asp	Leu	Gln	Gln	Ile
115							120						125		

Ile Val Ser Leu Thr Glu Ser Cys Arg Ser Cys Ser His Ala Leu Ala
 130 135 140

Ala His Val Ser His Leu Glu Asn Val Ser Glu Glu Glu Met Asn Arg
145 150 155 160

Leu Leu Gly Ile Val Leu Asp Val Glu Tyr Leu Phe Thr Cys Val His
165 170 175

Lys Glu Glu Asp Ala Asp Thr Lys Gln Val Tyr Phe Tyr Leu Phe Lys
180 185 190

Leu Leu Arg Lys Ser Ile Leu Gln Arg Gly Lys Pro Val Val Glu Gly
195 200 205

Ser Leu Glu Lys Lys Pro Pro Phe Glu Lys Pro Ser Ile Glu Gln Gly
210 215 220

Val Asn Asn Phe Val Gln Tyr Lys Phe Ser His Leu Pro Ala Lys Glu
225 230 235 240

Arg Gln Thr Ile Val Glu Leu Ala Lys Met Phe Leu Asn Arg Ile Asn
245 250 255

Tyr Trp His Leu Glu Ala Pro Ser Gln Arg Arg Leu Arg Ser Pro Asn
260 265 270

Asp Asp Ile Ser Gly Tyr Lys Glu Asn Tyr Thr Arg Trp Leu Cys Tyr
275 280 285

Cys Asn Val Pro Gln Phe Cys Asp Ser Leu Pro Arg Tyr Glu Thr Thr
290 295 300

Gln Val Phe Gly Arg Thr Leu Leu Arg Ser Val Phe Thr Val Met Arg
305 310 315 320

Arg Gln Leu Leu Glu Gln Ala Arg Gln Glu Lys Asp Lys Leu Pro Leu
325 330 335

Glu Lys Arg Thr Leu Ile Leu Thr His Phe Pro Lys Phe Leu Ser Met
340 345 350

Leu Glu Glu Val Tyr Ser Gln Asn Ser Pro Ile Trp Asp Gln Asp
355 360 365

Phe Leu Ser Ala Ser Ser Arg Thr Ser Gln Leu Gly Ile Gln Thr Val
370 375 380

Ile Asn Pro Pro Pro Val Ala Gly Thr Ile Ser Tyr Asn Ser Thr Ser
385 390 395 400

Ser Ser Leu Glu Gln Pro Asn Ala Gly Ser Ser Ser Pro Ala Cys Lys
405 410 415

Ala Ser Ser Gly Leu Glu Ala Asn Pro Gly Glu Lys Arg Lys Met Thr
420 425 430

Asp Ser His Val Leu Glu Glu Ala Lys Lys Pro Arg Val Met Gly Asp
435 440 445

Ile Pro Met Glu Leu Ile Asn Glu Val Met Ser Thr Ile Thr Asp Pro
450 455 460

Ala Ala Met Leu Gly Pro Glu Thr Asn Phe Leu Ser Ala His Ser Ala
465 470 475 480

Arg Asp Glu Ala Ala Arg Leu Glu Glu Arg Arg Gly Val Ile Glu Phe
485 490 495

His Val Val Gly Asn Ser Leu Asn Gln Lys Pro Asn Lys Lys Ile Leu
500 505 510

Met Trp Leu Val Gly Leu Gln Asn Val Phe Ser His Gln Leu Pro Arg
515 520 525

Met Pro Lys Glu Tyr Ile Thr Arg Leu Val Phe Asp Pro Lys His Lys
530 535 540

Thr Leu Ala Leu Ile Lys Asp Gly Arg Val Ile Gly Gly Ile Cys Phe
545 550 555 560

Arg Met Phe Pro Ser Gln Gly Phe Thr Glu Ile Val Phe Cys Ala Val
565 570 575

Thr Ser Asn Glu Gln Val Lys Gly Tyr Gly Thr His Leu Met Asn His
580 585 590

Leu Lys Glu Tyr His Ile Lys His Asp Ile Leu Asn Phe Leu Thr Tyr
595 600 605

Ala Asp Glu Tyr Ala Ile Gly Tyr Phe Lys Lys Gln Gly Phe Ser Lys
610 615 620

Glu Ile Lys Ile Pro Lys Thr Lys Tyr Val Gly Tyr Ile Lys Asp Tyr
625 630 635 640

Glu Gly Ala Thr Leu Met Gly Cys Glu Leu Asn Pro Arg Ile Pro Tyr
645 650 655

Thr Glu Phe Ser Val Ile Ile Lys Lys Gln Lys Glu Ile Ile Lys Lys
660 665 670

Leu Ile Glu Arg Lys Gln Ala Gln Ile Arg Lys Val Tyr Pro Gly Leu
675 680 685

Ser Cys Phe Lys Asp Gly Val Arg Gln Ile Pro Ile Glu Ser Ile Pro
690 695 700

Gly Ile Arg Glu Thr Gly Trp Lys Pro Ser Gly Lys Glu Lys Ser Lys
705 710 715 720

Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser Ile Leu
725 730 735

Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu Pro Val
740 745 750

Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Phe Pro Met
755 760 765

Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr Val Ser
770 775 780

Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys
785 790 795 800

Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu
805 810 815

Glu Lys Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys
820 825 830

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic bromodomain peptide

<220>
<221> Xaa
<222> (2)..(4)
<223> Xaa is a maximum of three amino acids. Each of these can be
any amino acid. One may be missing.

<220>
<221> Xaa
<222> (4)..(11)
<223> Xaa is a maximum of eight amino acids. Each of these can be
any amino acid. One, two, or three may be missing.

<220>
<221> Xaa
<222> (5)..(5)
<223> Xaa is a single amino acid that is either Pro, Lys, or His.

<220>
<221> Xaa
<222> (6)..(6)
<223> Xaa is any single amino acid.

<220>
<221> Xaa
<222> (8)..(8)
<223> Xaa is a single amino acid that can be either Tyr, Phe, or His.

<220>
<221> Xaa
<222> (9)..(13)
<223> Xaa is any amino acid.

<220>
<221> Xaa
<222> (15)..(15)
<223> Xaa is a single amino acid that can be either Met, Ile, or Val.

<400> 3

Phe Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp
1 5 10 15

<210> 4
<211> 12
<212> PRT
<213> Artificial Sequence
<220>
<223> synthetic bromodomain peptide

<220>
<221> Xaa
<222> (6)..(6)
<223> Xaa represents an acetyl-lysine

<400> 4

Ile Ser Tyr Gly Arg Xaa Lys Arg Arg Gln Arg Arg
1 5 10

<210> 5
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic bromodomain peptide

<220>
<221> Xaa
<222> (8)..(8)
<223> Xaa represents an acetyl lysine.

<400> 5

Ala Arg Lys Ser Thr Gly Gly Xaa Ala Pro Arg Lys Gln Leu
1 5 10

<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (8)...(8)

<223> Xaa represents an acetyl lysine.

<400> 6

Gln Ser Thr Ser Arg His Lys Xaa Leu Met Phe Lys Thr Glu
1 5 10

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

<400> 7

Ser Lys Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser
1 5 10 15

Ile Leu Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu
20 25 30

Pro Val Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Ser
35 40 45

Pro Met Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr
50 55 60

Val Ser Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn
65 70 75 80

Cys Lys Glu Tyr Asn Ala Pro Glu Ser Glu Tyr Tyr Lys Cys Ala Asn
85 90 95

Ile Leu Glu Lys Phe Phe Ser Lys Ile Lys Glu Ala Gly
100 105 110

<210> 8

<211> 110

<212> PRT

<213> Homo sapiens

<400> 8

Gly Lys Glu Leu Lys Asp Pro Asp Gln Leu Tyr Thr Thr Leu Lys Asn
1 5 10 15

Leu Leu Ala Gln Ile Lys Ser His Pro Ser Ala Trp Pro Phe Met Glu
20 25 30

Pro Val Lys Lys Ser Glu Ala Pro Asp Tyr Tyr Glu Val Ile Arg Phe

35

40

45

Pro Ile Asp Leu Lys Thr Met Thr Glu Arg Leu Arg Ser Arg Tyr Tyr

50

55

60

Val Thr Arg Lys Leu Phe Val Ala Asp Leu Gln Arg Val Ile Ala Asn

65

70

75

80

Cys Arg Glu Tyr Asn Pro Pro Asp Ser Glu Tyr Cys Arg Cys Ala Ser

85

90

95

Ala Leu Glu Lys Phe Phe Tyr Phe Lys Leu Lys Glu Gly Gly

100

105

110

<210> 9

<211> 109

<212> PRT

<213> Tetrahymena thermophila

<400> 9

Leu Lys Lys Ser Lys Glu Arg Ser Phe Asn Leu Gln Cys Ala Asn Val

1

5

10

15

Ile Glu Asn Met Lys Arg His Lys Gln Ser Trp Pro Phe Leu Asp Pro

20

25

30

Val Asn Lys Asp Asp Val Pro Asp Tyr Tyr Asp Val Ile Thr Asp Pro

35

40

45

Ile Asp Ile Lys Ala Ile Glu Lys Lys Leu Gln Asn Asn Gln Tyr Val

50

55

60

Asp Lys Asp Gln Phe Ile Lys Asp Val Lys Arg Ile Phe Thr Asn Ala

65

70

75

80

Lys Ile Tyr Asn Gln Pro Asp Thr Ile Tyr Tyr Lys Ala Ala Lys Glu

85

90

95

Leu Glu Asp Phe Val Glu Pro Tyr Leu Thr Lys Leu Lys

100

105

<210> 10

<211> 109

<212> PRT

<213> Saccharomyces cerevisiae

<400> 10

Ala Gln Arg Pro Lys Arg Gly Pro His Asp Ala Ala Ile Gln Asn Ile

1

5

10

15

Leu Thr Glu Leu Gln Asn His Ala Ala Ala Trp Pro Phe Leu Gln Pro

20

25

30

Val Asn Lys Glu Glu Val Pro Asp Tyr Tyr Asp Phe Ile Lys Glu Pro
35 40 45

Met Asp Leu Ser Thr Met Glu Ile Lys Leu Glu Ser Asn Lys Tyr Gln
50 55 60

Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys
65 70 75 80

Arg Met Tyr Asn Gly Glu Asn Thr Ser Tyr Tyr Lys Tyr Ala Asn Arg
85 90 95

Leu Glu Lys Phe Phe Asn Asn Lys Val Lys Glu Ile Pro
100 105

<210> 11
<211> 112
<212> PRT
<213> Homo sapiens

<400> 11

Lys Lys Ile Phe Lys Pro Glu Glu Leu Arg Gln Ala Leu Met Pro Thr
1 5 10 15

Leu Glu Ala Leu Tyr Arg Gln Asp Pro Glu Ser Leu Pro Phe Arg Gln
20 25 30

Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr Phe Asp Ile Val
35